

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:26:06 ; Search time 0.001 Seconds  
 (without alignments)  
 143.112 Million cell updates/sec

Title: us-10-088-666-1  
 Perfect score: 267  
 Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 13 seqs, 268 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 300 summaries

Database : rgedb1:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
				DB			
1	25	9.4	25	1	AX105801	ACCESSION:AX105801	
2	25	9.4	25	1	AX105830	ACCESSION:AX105830	
c 3	23	8.6	23	1	AX105781	ACCESSION:AX105781	
4	21	7.9	21	1	AX105749	ACCESSION:AX105749	
5	21	7.9	21	1	AX105827	ACCESSION:AX105827	
6	20	7.5	20	1	AR105913	ACCESSION:AR105913	
7	20	7.5	20	1	E04248	ACCESSION:E04248	
8	20	7.5	20	1	E07340	ACCESSION:E07340	
9	20	7.5	20	1	E07586	ACCESSION:E07586	
10	20	7.5	20	1	AX105802	ACCESSION:AX105802	
11	20	7.5	20	1	AX105826	ACCESSION:AX105826	
c 12	18	6.7	18	1	AX105791	ACCESSION:AX105791	
c 13	15	5.6	15	1	AR371336	ACCESSION:AR371336	
c 14	11	4.1	21	1	AX105749	ACCESSION:AX105749	
c 15	8.2	3.1	25	1	AX105801	ACCESSION:AX105801	
c 16	7.8	2.9	25	1	AX105830	ACCESSION:AX105830	
c 17	7.4	2.8	20	1	AX105802	ACCESSION:AX105802	

c	18	7.2	2.7	20	1	AR105913	ACCESSION:AR105913
c	19	7.2	2.7	20	1	E04248	ACCESSION:E04248
c	20	7.2	2.7	20	1	E07340	ACCESSION:E07340
c	21	7.2	2.7	20	1	E07586	ACCESSION:E07586
c	22	7.2	2.7	21	1	AX105827	ACCESSION:AX105827
	23	6.8	2.5	23	1	AX105781	ACCESSION:AX105781
	24	6.2	2.3	15	1	AR371336	ACCESSION:AR371336
	25	6	2.2	18	1	AX105791	ACCESSION:AX105791
c	26	5.8	2.2	20	1	AX105826	ACCESSION:AX105826

OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:28:05 ; Search time 0.001 Seconds  
 (without alignments)  
 106.800 Million cell updates/sec

Title: us-10-088-666-1  
 Perfect score: 267  
 Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 200 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 300 summaries

Database : rnpbndb1:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	25	9.4	25	1	US-11-348-413-350688	Sequence 350688,	
2	25	9.4	25	1	US-11-348-413-350689	Sequence 350689,	
3	25	9.4	25	1	US-11-348-413-988351	Sequence 988351,	
4	25	9.4	25	1	US-11-348-413-988352	Sequence 988352,	
5	25	9.4	25	1	US-11-348-413-988353	Sequence 988353,	
6	25	9.4	25	1	US-11-348-413-988354	Sequence 988354,	
7	25	9.4	25	1	US-11-348-413-988355	Sequence 988355,	
8	25	9.4	25	1	US-11-348-413-988356	Sequence 988356,	
c 9	6.6	2.5	25	1	US-11-348-413-350688	Sequence 350688,	
c 10	6.6	2.5	25	1	US-11-348-413-350689	Sequence 350689,	
c 11	6.6	2.5	25	1	US-11-348-413-988352	Sequence 988352,	
c 12	6.6	2.5	25	1	US-11-348-413-988353	Sequence 988353,	
c 13	6.6	2.5	25	1	US-11-348-413-988354	Sequence 988354,	
c 14	6.6	2.5	25	1	US-11-348-413-988355	Sequence 988355,	
c 15	6.6	2.5	25	1	US-11-348-413-988356	Sequence 988356,	
c 16	6.2	2.3	25	1	US-11-348-413-988351	Sequence 988351,	

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:27:26 ; Search time 0.001 Seconds  
(without alignments)  
18.690 Million cell updates/sec

Title: us-10-088-666-1  
Perfect score: 267  
Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 35 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : rnidb1:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	20	7.5	20	1	US-08-944-974A-1	Sequence 1, Appli
c	2	15	5.6	15	1	US-08-461-210-30	Sequence 30, Appl
c	3	7.2	2.7	20	1	US-08-944-974A-1	Sequence 1, Appli
	4	6.2	2.3	15	1	US-08-461-210-30	Sequence 30, Appl